RESULT 4 ECNRFA

BCT 06-JUN-1995

LOCUS DEFINITION ACCESSION

VERSION KEYWORDS

SOURCE

ECNRFA 7320 bp DNA linear BCT 06-JUN-19
E.coli nrfA gene.
X72298
X72298.1 GI:404302
cytochrome c-552; nitrite reductase; nrfA gene.
Escherichia coli.
Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.

ORGANISM

REFERENCE AUTHORS

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

1 (bases 1 to 7320)
Darwin,A., Hussain,H., Griffiths,L., Grove,J., Sambongi,Y.,
Busby,S. and Cole,J.
Regulation and sequence of the structural gene for cytochrome c552
from Escherichia coli: not a hexahaem but a 50 kDa tetrahaem

TITLE

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REFERENCE
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TITLE
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-MAY-1993)
School of Biochemistry,
revised by [3]
3 (bases 1 to 7320)
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Direct Submission
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BASE COUNT
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Best Local :
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CTACTTCAAGGGCAAGGAGAAGCGCCTCACGTACCCCTGGGCCAAGGGGCATCAACATCGA 833
                                                 TGAGAAAGCCGGACGTTTCGACCAGCAATCGATGGTTTGCGGTCAGTGCCATGTGGAGTA 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="hydrophobic protein of unknown function"
                                                                                                                                                                                   7.5%;
                                                                                                                                                          Score 111.6; DB 1 pred. No. 2.7e-05; 0; Mismatches 314
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Db	950		1009
Qу	834	TCAGATCATGGCCTACTACGACGAGGACGACACTCCGACTGGACGCACGAGCTCACGGG	893
Db	1010	AAATATGGAGCAGTATTACGACAAAATTGCCTTCTCTGACTGGACTAACTCCCTGTCGAA	1069
Qу	894	CGCCAAGGTGCTGAAGCCCCGAGTTCGAGATGTACAACCAGGGCATCCACGC	953
Db	1070	AACGCCAATGCTGAAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTCACGG	1129
Qy	954	GAAGAGCGGCGTGGCCTGCGGGACTGCCACATGCCGTTCATGCGCGAGGGGGCGATGAA	1013
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RESULT 7
 ECNRFA
 LOCUS
                     ECNRFA
                                                             7320 bp
                                                                                DNA
                                                                                             linear
                                                                                                             BCT 06-JUN-1995
 DEFINITION
                     E.coli nrfA gene.
X72298
 ACCESSION
 VERSION
                     X72298.1 GI:404302
 KEYWORDS
                     cytochrome c-552; nitrite reductase; nrfA gene. Escherichia coli.
 SOURCE
    ORGANISM
                     Escherichia coli
                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
 REFERENCE
                     1 (bases 1 to 7320)
                     Darwin, A., Hussain, H., Griffiths, L., Grove, J., Sambongi, Y., Busby, S. and Cole, J.
    AUTHORS
                     Regulation and sequence of the structural gene for cytochrome c552 from Escherichia coli: not a hexahaem but a 50 kDa tetrahaem
    TITLE
                     nitrite reductase
    JOURNAL
                     Mol. Microbiol. 9 (6), 1255-1265 (1993) 95020657
    MEDLINE
     PUBMED
                     7934939
REFERENCE
                    2 (bases 1 to 7320)
Hussain, H.A.
   AUTHORS
    TITLE
                    Direct Submission
                    Submitted (28-MAY-1993) H.A. Hussain, University of Birmingham, School of Biochemistry, Edgbaston, Birmingham, B15 2TT, UK
   JOURNAL
                    revised by [3]
3 (bases 1 to 7320)
   REMARK
REFERENCE
   AUTHORS
                    Hussain, H.A.
                   Hussain, H.A.
Direct Submission
Submitted (29-SEP-1993) H.A. Hussain, University of Birmingham,
School of Biochemistry, Edgbaston, Birmingham, B15 2TT, UK
On Sep 30, 1993 this sequence version replaced gi:312132.
   TITLE
   JOURNAL
COMMENT
                                  0, 1993 this sequence version Location/Qualifiers
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capsulatus"
                                                                                                                                                                                                                                                                                                                                                                                  4051
                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT: P32709"
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3015. .3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="miwsrropligylaavsgtagrvvaktlningvrygmyhdes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="nrfB"
1784 . .2350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3015. .3971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="GI:404305"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to NADH ubiquinone oxidoreductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS-PROT:P32708"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-PROT: B32707"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="member of coof family containing 4Fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="nrfC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KICVDCHSDQRTNPNFNPASVPLLKEQP"
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                                                                                                                                                                                                                                                                          ccll protein from Rhodobacter
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                666
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                                                         157
                                                                                                      909
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US-09-902-540-11926 (1-494) x ECNRFA (1-7320)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                        123 TyrAlaPheAlaThrAspPheArgGluGluArgGlyHisAlaHisMetLeuAspAspGln 142
                                                                                                                                                                                                                                                                                                                                                                                           432 ACCTTTGCCCCGCAGCATCCCGATCAATATCTCTCCTGGAAAGCCACCTCGGAACAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 GAAGCGAAGAAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                63 ValTrpGlyArgAsnPhcProLeuGlnTyrAspSerTyrLysArgThrValAspGlnGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 GlualaLysasnProPheTyrArgValValGluLeuAspAspThrIleThrAspProGlu 62
                                 CysIleHisCysHisAlaSerValTyrValProTyrLysLysLeuGlyAspGlyAspLeu 176
                                                                                                                    ValTyrThrGluArgGlnHisValThrGlnGln--
        TGCTGGAGTTGTAAAAGCCCG--
                                                                      CGTGAAACCCTGCGTACCGGTGCGCCGAAAAACGCTGAAGATGGTCCGCTACCGATGGCA 665
                                                                                                                                                     TATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTTGCTGTGACCGATGTG
                                                                                                                                                                                                                                                                                                                                                 ArgThrArgTyrGlyGlySerGluAlaValAlaArgThrProSerGlnAlaAspProArg
                                                                                                                                                                                                                                                        ThrValValAlaGInSerArgLeuGluGluAspProArgLeuValThrMetTrpSerGly 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1621
                                                                                                                                                                                                                               ------GACGCCCTGGCGGAAGATCCACGGCTGGTGATCCTGTGGGCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQAIELWQKVMDLNSPRVNRTQLVESINMAKLLQRRLD"
1847 c 2071 g 1781 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mnkglltllllftcfahaqvvdtmofandqqqqalniasqlrc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hydrophobic protein of unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVLWALPVVLLLLMALILWRVRAKR"
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capsulatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nrff"
5702. .6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKTGPDRYAFRLYVQSGVRWIWGGGLLMIAGALLSGWRGKKRDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LATLLLECAVLLIVLVGTLYPMIYGLLGWGRLSVGAPYFNRATLPEGLLMLVVIVLAT
FVSGKRVQLPALVAHAGVLLEAAGVVVSSVSRQEISLNLQPGQQVTLAGYTEREECLD
LQAKANYTSEKAIVALFDHQQRIGELTPERAFYEARRQQMMEPSIRWNGIHDWYAVMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="nrfF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="SWISS-PROT:P32711"
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29.48%
19.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.3e-31
506.50
                                                                                                                                                                                                                                                                                                                           TCAGAGCGTGTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to cc12 protein from Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
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135
71
152
101
                                                                                                               ProGlyThr 156
GATGTG
692
                                                                                                                                                       605
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                                                                                                                                                                                                                                                                                                                500
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us-09-902-5

## Tue Nov 12 08:22:12 2002

Qу	177	IleLysGlyPheGluLysMetAsnGlnMetProPheMetGluAlaArg	192
Db	693		752
Qу	193	LysLeuValGluHisProValSerCysIleAspCysHisAspProThrThr :::::  -  :::   -    -    -    -	209
Db	753	GGTCCGGAAATCGTCAACAAC TTAGGTTGTGCCGATTGCCATAACACCGCCTCTCCA	809
Qу	210	MetGlnLeuArgValThrArgProGlyPheIleGluGlyIle :::    :::::	223
Db	810	:::    ::::::       ::: GAGTTCGCCAAAGGCAAACCGGAGTTAACCCTTTCCCGTCCGT	869
Qy	224		243
Db	870	ATAATALEUUTSATASETTIIGT VATTOON TEETINGATAATALEUUTSATASETTIIGT TITTIIGAGAAAGCCGACGT	905
Qу	244	GlnGluMetArgThrTyrValCysGlyGlnCysHisValGluTyrTyrPheLysGlyLys	263
Db	906	TTCGACCAGCAATCGATGGTTTGCGGTCAGTGCCATGTGGAGTATTACTTCGACGGCAAA	965
Qy	264	GluLysArgLeuThrTyrProTrpAlaLysGlyIleAsnIleAspGlnIleMetAlaTyr	283
Db		AACAAAGCGGTTAAATTCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAGTAT	1025
Qу	284	TyrAspGluAspGlyHisSerAspTrpThrHisGluLeuThrGlyAlaLysValteuLys	303
Db		TACGACAAAATTGCCTTCTCTGACTGGACTAACTCCCTGTCGAAAACGCCAATGCTGAAA	
QУ		AlaGlnHisProGluPheGluMetTyrAsnGlnGlyIleHisAlaLysSerGlyValAla	
Db		GCGCAGCACCCGGAAFATGAAACCTGGACAGCGGGCATTCACGGTAAAAACAACGTGACC	
Qу		CysAlaAspCysHisMetProPheMetArgGluGlyAlaMetLysValSerAspHis	
Db		TGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAGGCAAACTCTACACCGACCAT	
Qy		GlnvalArgSerProLeuLeuAsnIleAsnArgAlaCysGlnThrCysHisLysTrpSer	
Db		AAAATTGGTAATCCGTTTGATAACTTCGCCCAGACTTGTGCGAACTGCCATACCCAGGAC	
Qу		GluAlaGluLeuLeuGlnArgAlaGluThrIleGlnThrArgThrPhe	
Db		AAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGCAGTCGATTAACGACCTGAAAATC	
Qу		GluThrArgAsnIleAlaMetAspAlaLeuValAspLeuIleHisAspIleGluAlaAla	
Db	1326	5 AAGGTTGAAGATCAACTGGTTCACGCTCACTTCGAAGUGAAAGUAGU	
Qy	399	GlnLysAlaGlyGlnSerGluGluAlaLeuAlaLysAlaArgAspLeuGlnLysArgAla	
Db		4 CTGGATGCAGGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATATCCGTCATGCC	. 1433
Qу		9 GlnPheTyrLeuAspPheValGluAlaGluAsnSerMetGlyPheHisAlaAspGlnGlu	
Db		4 CAGTGGCGCTGGGATCTGGCGATCGCTTCCCACGGCATTCATATGCACGCAC	1493
QУ		9 AlaValArgIleLeuSerAsnSerIleAsnPheSerArgLeuGlyGlnAsnAlaLeuArg ::::   :::	
Db		4 GGTTTACGGATGCTCGGTACGGCGATGGAT	. 152
QУ	45	9 ProSerGlyGlyAlaSerThrSerProThrThrArgProGlnGlyAlaProAla 476           4 AA-AGCGGCGGATGCACGCACCAAACTGGCGCGCCTGCT 1561	
Db	152	4 AA-AGCGGCGGATGCACGCACCAAACTGGCGCGCCTGCT 1561	